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## RAW SEQUENCE LISTING

DATE: 02/06/2002

PATENT APPLICATION: US/10/014,156

TIME: 09:40:49

Input Set : N:\Crf3\RULE60\10014156.raw

Output Set: N:\CRF3\02062002\J014156.raw

ENTERED

1 <110> APPLICANT: Hilton, Douglas J.  
 2 Willson, Tracy  
 3 Nicola, Nicos A.  
 4 Gainsford, Timothy  
 5 Alexander, Warren S.  
 6 Metcalf, Donald  
 7 Ng, Ashley  
 8 <120> TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES  
 9 ENCODING SAME  
 10 <130> FILE REFERENCE: 11268  
 12 <140> CURRENT APPLICATION NUMBER: 10/014,156  
 13 <141> CURRENT FILING DATE: 2001-12-07  
 15 <150> PRIOR APPLICATION NUMBER: US/09/043,816  
 16 <151> PRIOR FILING DATE: 1998-09-17  
 19 <160> NUMBER OF SEQ ID NOS: 44  
 20 <170> SOFTWARE: PatentIn Ver. 2.0  
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 23 <211> LENGTH: 15  
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 25 <213> ORGANISM: Artificial Sequence  
 26 <220> FEATURE:  
 27 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
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 35 <220> FEATURE:  
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 38 taatacgact cactataggg aga 23  
 40 <210> SEQ ID NO: 3  
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 50 <211> LENGTH: 21  
 51 <212> TYPE: DNA

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52 <213> ORGANISM: Artificial Sequence
53 <220> FEATURE:
54 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic
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62 <220> FEATURE:
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65     ctcagctaca tccctgctag t                                21
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68 <211> LENGTH: 17
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71 <220> FEATURE:
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89 <220> FEATURE:
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104 <211> LENGTH: 34
105 <212> TYPE: DNA
106 <213> ORGANISM: Artificial Sequence

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116 <220> FEATURE:
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123 <212> TYPE: DNA
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127 <222> LOCATION: (27)..(68)
128 <223> OTHER INFORMATION: N is a or g or c or t
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130 <222> LOCATION: (923)
131 <223> OTHER INFORMATION: R is g or a
132 <221> NAME/KEY: unsure
133 <222> LOCATION: (2315)
134 <223> OTHER INFORMATION: S is g or c
135 <400> SEQUENCE: 12
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W--> 137      ctctgtggnat tatecttcag tggggstatt ggactgactt ttcttatgct gggatgtgcc 120
138      ttagaggatt atggatttgg cagttcaccc tgaccatctt gaaaataagt tatctctgat 180
139      ctctgtctgt atgttacttc tctccctcca ccaacggaga acaaagtgg gcaaagtga 240
140      cttctctgaa gtaagatgat ttgtcaaaaa ttctgtgtgg ttttgttaca ttgggaattt 300
141      atttatgtga taactgcgtt taacttgtca tatccaatta ctcttgagg attttaagttg 360
142      tcttgcattg caccaaattc aacctatgac tacttccctt tgcttgcctg actctcaaag 420
143      aataacttcaa attcgaatgg acattatgag acagctgttg aacctaaagt taattcaagt 480
144      ggtactcact tttctaactt atccaaaaca actttccact gttgctttcg gagtgcagca 540
145      gatagaaact gctccttatg tgcagacaac attgaaggaa ggacatttgt ttcaacagta 600
146      aattcttttag tttttcaaca aatagatgca aactggaaca tacagtgcct gctaaaagga 660
147      gacttaaaat tattcatctg ttatgtggag tcattattta agaatctatt caggaattat 720
148      aactataagg tccatctttt atatgttctg cctgaagtgt tagaagattc acctctggtt 780
149      ccccaaaaag gcagttttca gatggttcac tgcaattgca gtgttcattga atgttgtgaa 840
150      tgtcttgtgc ctgtgccaac agccaaactc aacgacactc tccttatgtg ttgaaaatc 900
151      acatctgggt gagtaatttt ccrgtcacct ctaatgtcag ttcagcccat aaatatggtg 960
152      aagcctgac caccattagg tttgcatatg gaaatcacag atgatggtaa tttaaagatt 1020
153      tcttgggtcca gccaccattt ggtaccattt ccacttcaat atcaagtga atattcagag 1080
154      aattctacaa cagttatcag agaagctgac aagattgtct cagctacatc cctgctagta 1140
155      gacagtatac ttcttggttc ttcgtatgag gttcagggtga ggggcaagag actggatggc 1200
156      ccaggaatct ggagtgcact gagtactcct cgtgtcttta ccacacaaga tgtcatatac 1260
157      tttccaccta aaattctgac aagtgttggg tctaattgtt cttttcactg catctataag 1320

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158      aaggaaaaca agattgttcc ctcaaaagag attgtttggt ggatgaattt agctgagaaa 1380
159      attcctcaaa gccagtatga tgttgtgagt gatcatgtta gcaaagtac ttttttcaat 1440
160      ctgaatgaaa ccaaacctcg aggaaagttt acctatgatg cagtgtactg ctgcaatgaa 1500
161      catgaatgcc atcatcgcta tgctgaatta tatgtgattg atgtcaatat caatatctca 1560
162      tgtgaaactg atgggtactt aactaaaatg acttgcagat ggtcaaccag tacaatccag 1620
163      tcacttgcgg aaagcacttt gcaattgagg tatcatagga gcagccttta ctgttctgat 1680
164      attccatcta ttcattcccat atctgagccc aaagattgct atttgcagag tgatggtttt 1740
165      tatgaatgca ttttccagcc aatcttcccta ttatctggct acacaatgtg gattaggatc 1800
166      aatcactctc taggttccact tgactctcca ccaacatgtg tccttcccta ttctgtggtg 1860
167      aagccactgc ctccatccag tgtgaaagca gaaattacta taaacattgg attattgaaa 1920
168      atatcttggg aaaagccagt ctttccagag aataaccttc aattccagat tcgctatggt 1980
169      ttaagtggaa aagaagtaca atggaagatg tatgaggttt atgatccaaa accaaaatct 2040
170      gtcagtctcc cagttccaga cttgtgtgca gtctatgctg ttcagggtggc gtttaagagg 2100
171      ctagatggac tgggatattg gagtaattgg agcaatccag cctacacagt tgtcatggat 2160
172      ataaaagttc ctatgagagg acctgaattt tggagaataa ttaatggaga tactatgaaa 2220
173      aaggagaaaa atgtcacttt actttggaag cccctgatga aaaatgactc attgtgcagt 2280
174      gttcagagat atgtgataaa ccatcatact tcctscatg gaacatgggtc agaagatgtg 2340
175      ggaaatcaca cgaaattcac tttcctgtgg acagagcaag cacatactgt tacggttctg 2400
176      gccatcaatt caattggtgc ttctgttgca aattttaatt taaccttttc atggcctatg 2460
177      agcaaagtaa atatcgtgca gtcactcagt gcttatcctt taaacagcag ttgtgtgatt 2520
178      gtttctgga tactatcacc cagtgttacc aagctaattg attttattat tgatggaaa 2580
179      aatcttaatg aagatggtga aataaaatgg cttagaatct cttcatctgt taagaagtat 2640
180      tatatccatg atcatcttat cccattgag aagtaccagt tcagtcttta cccaatattt 2700
181      atggaaggag tgggaaaacc aaagataatt aatagtttca ctcaagatga tattgaaaaa 2760
182      caccagagtg atgcaggttt atatgtaatt gtgccagtaa ttatttcctc ttccatctta 2820
183      ttgcttgga cattaatta atcacaccaa agaataaaaa agctattttg ggaagatgtt 2880
184      ccgaaccca agaattgttc ctgggcacaa ggacttaatt ttcagaagag aacggacatt 2940
185      ctttgaagtc taatcatgat cactacagat gaaccaatg tgccaacttc ccaacagtct 3000
186      atagagtatt agaagatttt tacattttga agaaggggag caaatctaaa aaaaattcag 3060
187      ttgaacttct gagagttaac atatggtgga ttatgttgat ttagaactta aaatagatgt 3120
188      catttaaacc caagttttac atctaaactc aggtcaaacc tacacactaa ttaaaagttt 3180
189      agtagatttc aaattttcat cafaagtact aaagaccgaa aactaaacag tataaggacc 3240
190      agtattttgt aattctttta ataccgacaa cgacagtaat gtatagataa ttacagtag 3300
191      tttatacatc atctgttagg acattaatcc acttgagatt ttgacgttgt agactgttta 3360
192      tcgaaatttt tatgttacta atattcatac cttagtcact tttataaatc aaacataaaa 3420
193      atacagttt gaaaaggtaa aatctaagga aatatctgtg cagtcggatt tttagtcgga 3480
194      taagcccaca agaaaactta tagaggaccg taaaaacata gattgaaaca agttagacc 3540
195      ttaaagtcaa agtttatagg aacttttacc gaattcacta ttgaaggcaa agtcaatttt 3600
196      ccttcgggct tcaacacaaa cagcagcggg gtccgtgcac cctcaatgtc aagtatagtc 3660
197      ctactgggat gtatgggtcc agtctaactg ccctgggtct ccctgttagc tgaagattac 3720
198      aggtgcgaaa gaacaaatta atactggatt tagattaaat gaagtgactc tggtaggttc 3780
199      tggagaccgt ccgtcccttt acccgtaact asgttttttc cctctgagaa acctcgaaaa 3840
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201      atacttaag
203 <210> SEQ ID NO: 13
204 <211> LENGTH: 896
205 <212> TYPE: PRT
206 <213> ORGANISM: Homo sapiens
207 <220> FEATURE:

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Input Set : N:\Crf3\RULE60\10014156.raw

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208 <221> NAME/KEY: UNSURE
209 <222> LOCATION: (223)
210 <223> OTHER INFORMATION: Xaa is unknown or other.
211 <221> NAME/KEY: UNSURE
212 <222> LOCATION: (687)
213 <223> OTHER INFORMATION: Xaa is unknown or other.
214 <400> SEQUENCE: 13
215 Met Ile Cys Gly Lys Phe Cys Val Val Leu Leu His Trp Gln Phe Ile
216 1 5 10 15
217 Tyr Val Ile Thr Ala Phe Asn Leu Ser Tyr Pro Ile Thr Pro Trp Arg
218 20 25 30
219 Phe Lys Leu Ser Cys Met Pro Pro Asn Ser Thr Thr Asn Tyr Phe Leu
220 35 40 45
221 Leu Pro Ala Gly Leu Ser Lys Asn Thr Ser Asn Ser Asn Gly His Tyr
222 50 55 60
223 Glu Thr Ala Val Glu Pro Lys Phe Asn Ser Ser Gly Thr His Phe Ser
224 65 70 75 80
225 Asn Leu Ser Lys Thr Thr Phe His Cys Cys Phe Arg Ser Glu Gln Asp
226 85 90 95
227 Arg Asn Cys Ser Leu Cys Ala Asp Asn Ile Glu Gly Arg Thr Phe Val
228 100 105 110
229 Ser Thr Val Asn Ser Leu Val Phe Gln Gln Ile Asp Ala Asn Trp Asn
230 115 120 125
231 Ile Gln Cys Trp Leu Lys Gly Asp Leu Lys Leu Phe Ile Cys Tyr Val
232 130 135 140
233 Glu Ser Leu Phe Lys Asn Leu Phe Arg Asn Tyr Asn Tyr Lys Val His
234 145 150 155 160
235 Leu Leu Tyr Val Leu Pro Glu Val Leu Glu Asp Ser Pro Leu Val Pro
236 165 170 175
237 Gln Lys Gly Ser Phe Gln Met Val His Cys Asn Cys Ser Val His Glu
238 180 185 190
239 Cys Cys Glu Cys Leu Val Pro Val Pro Thr Ala Lys Leu Asn Asp Thr
240 195 200 205
W--> 241 Leu Leu Met Cys Leu Lys Ile Thr Ser Gly Gly Val Ile Phe Xaa Ser
242 210 215 220
243 Pro Leu Met Ser Val Gln Pro Ile Asn Met Val Lys Pro Asp Pro Pro
244 225 230 235 240
245 Leu Gly Leu His Met Glu Ile Thr Asp Asp Gly Asn Leu Lys Ile Ser
246 245 250 255
247 Trp Ser Ser Pro Pro Leu Val Pro Phe Pro Leu Gln Tyr Gln Val Lys
248 260 265 270
249 Tyr Ser Glu Asn Ser Thr Thr Val Ile Arg Glu Ala Asp Lys Ile Val
250 275 280 285
251 Ser Ala Thr Ser Leu Leu Val Asp Ser Ile Leu Pro Gly Ser Ser Tyr
252 290 295 300
253 Glu Val Gln Val Arg Gly Lys Arg Leu Asp Gly Pro Gly Ile Trp Ser
254 305 310 315 320
255 Asp Trp Ser Thr Pro Arg Val Phe Thr Thr Gln Asp Val Ile Tyr Phe
256 325 330 335

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## VERIFICATION SUMMARY

DATE: 02/06/2002

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Output Set: N:\CRF3\02062002\J014156.raw

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L:241 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:441 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
L:619 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44